

TECHNICAL AMENDMENTS TO THE CLAIMS:**IN THE CLAIMS:**

Please cancel Claims 23-44 without disclaimer or prejudice to Applicants' right to pursue the subject matter of these claims in a future divisional or continuation application.

Please amend Claims 2-20, 22 and 46 as indicated hereinbelow.

1. (Previously amended) An isolated peptide comprising the peptide sequence of formula (I),

Xaa-Cys-Xab-Cys-Xac-Cys-Xad-Cys-Xae-Cys-Xaf-Cys-Xag (SEQ ID NO:39)

(I)

in which:

Xaa is $-\text{NH}_2$ or a peptide residue consisting essentially of from 1 to 10 amino acids; preferably from 1 to 6 amino acids;

Xab is a peptide residue consisting essentially of from 1 to 10 amino acids, preferably 10;

Xac is a peptide residue of 3 amino acids;

Xad is a peptide residue consisting essentially of from 1 to 9 amino acids, preferably 9;

Xae is a peptide residue consisting essentially of from 1 to 7 amino acids, preferably 7;

Xaf is a peptide residue of 1 amino acid; and

Xag is $-\text{OH}$ or a peptide residue consisting essentially of from 1 to 5 amino acids, preferably 1 or 2 amino acids.

2. (Currently Amended) The peptide of according to eClaim 1, wherein characterized in that

Xaa comprises at least one basic amino acid; and/or

Xad comprises at least one basic amino acid.

3. (Currently Amended) The peptide of according to eClaim 2, wherein characterized in that Xad comprises 1, 2, 3 or 4 basic amino acids.

4. (Currently amended) The peptide of according to eClaim 2, wherein characterized in that the basic amino acids are selected chosen from the group consisting of lysine, arginine or and homoarginine.

5. (Currently amended) The peptide according to of Celaim 1, characterized in that wherein Xad represents the following peptide sequence -Lys-Xad'-Xad"-Gly-His- (SEQ ID NO:40), in which Xad' represents a peptide residue of 1 basic amino acid and Xad" represents a peptide residue comprising from 0 to 5 amino acids, preferably 5.

6. (Currently amended) The peptide according to of Celaim 1, characterized in that wherein Xad represents the following peptide sequence -Lys-Arg-Arg-Gly-Tyr-Lys-Gly-Gly-His- (SEQ ID NO:41).

7. (Currently amended) The peptide according to one of Celaims 1to-6, characterized in that wherein Xac comprises at least one acidic amino acid, preferably 1.

8. (Currently amended) The peptide according to one of Celaim 1, characterized in that wherein Xac represents the following peptide sequence -Asn-Xac'-Xac"-, in which Xac' represents a peptide residue of 1 amino acid, and Xac" represents a peptide residue of 1 acidic amino acid.

9. (Currently amended) The peptide according to of Celaim 7, characterized in that the acidic amino acids are chosen from glutamic acid (Glu) or aspartic acid (Asp).

10. (Currently amended) The peptide according to of Celaim 1, characterized in that wherein Xac represents the following peptide sequence – Asn-Gly-Glu-.

11. (Currently amended) The peptide of Celaim 1, characterized in that wherein Xaa represents the following peptide sequence Xaa'-Gly-Xaa"- (SEQ ID NO:42), in which Xaa' represents NH₂ or a peptide residue comprising 1 to 9 amino acids, preferably 1 to 5 amino acids, and Xaa" represents a peptide residue comprising at least one amino acid, preferably chosen from Leu, Ile, Val, Pro, Ser or Thr;; and/or

Xab represents the following peptide sequence –Val-Xab'-Asp- (SEQ ID NO:43) in which Xab' represents a peptide residue comprising from 0 to 8 amino acids, preferably 8;; and/or

Xae represents the following peptide sequence –Gly-Xae'-Asn- (SEQ ID NO:44), in which Xae' represents a peptide residue comprising from 0 to 5 amino acids, preferably 5;; and/or

Xaf represents one of the following amino acids Trp, Phe, Leu, Ile or Val;; and/or

Xag represents the following peptide sequence –Glu-Xag' (SEQ ID NO:45), in which Xag' represents OH or a variable residue having a sequence comprising 1 to 4 amino acids, preferably 1 amino acid.

12. (Currently amended) The peptide according to of Celaim 1, characterized in that wherein Xaa represents the following peptide sequence NH₂-Asp-Lys-Leu-Ile-Gly-Ser- (SEQ ID NO:46);; and/or

Xab represents the following peptide sequence –Val-Trp-Gly-Ala-Val-Asn-Tyr-Thr-Ser-Asp- (SEQ ID NO:47);; and/or

Xae represents the following peptide sequence -Gly-Ser-Phe-Ala-Asn-Val-Asn (SEQ ID

NO:48); and/or

Xaf represents the following amino acid -Trp-; and/or

Xag represents the following peptide sequence -Glu-Thr-OH.

13. (Currently amended) The peptide according to of Celaim 1, characterized in that it wherein said peptide has the amino acid sequence encoded by is represented by the identifier No. 2 (SEQ ID NO:2).

14. (Currently amended) The peptide according to of Celaim 1, characterized in that it wherein said peptide comprises at either of its ends, or at both ends, peptide residues necessary for its expression and targeting in a host organism.

15. (Currently amended) The peptide according to of Celaim 1, characterized in that wherein the cysteine residues of the peptide of formula (I) form at least one intramolecular disulphide bridge.

16. (Currently amended) The peptide according to of Celaim 15, characterized in that it wherein said peptide comprises disulfide bridges established between the first and fourth cysteine residues, the second and fifth cysteine residues, and the third and sixth cysteine residues of the peptide sequence of formula (I).

17. (Currently amended) A "Peptide-heliomicine" fusion peptide, characterized in that comprising the heliomicine is a peptide of as defined according to eClaim 1.

18. (Currently amended) The ffusion peptide of according to eClaim 17, characterized in that wherein the peptide fused with heliomicine is comprises a signal peptide or a transit peptide.

19. (Currently amended) The fusion peptide of according to eClaim 18, characterized in that wherein the transit peptide is selected from the group consisting of the signal peptide of the tobacco PR-1 α gene, or the precursor of factor Mat alpha 1, or and the signal peptide of the maize polygalacturonase PG1 gene.

20. (Currently amended) The fusion peptide according to eClaim 19, characterized in that it is represented by the sequence identifier No. 1 (wherein the peptide has the amino acid sequence encoded by SEQ ID NO:1), by the sequence identifier No. 3 (SEQ ID NO:3), or by the sequence identifier No. 18 (SEQ ID NO:18).

21. (Cancelled).

22. (Currently amended) A composition, characterized in that it which comprises the peptide according to one of eClaim 1 and an appropriate vehicle.

23. (Cancelled).

24. (Cancelled).

25. (Cancelled).

26. (Cancelled).

27. (Cancelled).

28. (Cancelled).

29. (Cancelled).

30. (Cancelled).

31. (Cancelled).

32. (Cancelled).
33. (Cancelled).
34. (Cancelled).
35. (Cancelled).
36. (Cancelled).
37. (Cancelled).
38. (Cancelled).
39. (Cancelled).
40. (Cancelled).
41. (Cancelled).
42. (Cancelled).
43. (Cancelled).
44. (Cancelled).
45. (Cancelled).
46. (Currently amended) A method of preparing the peptide of Claim 1, ~~characterized in that it comprisesing the steps of~~ culturing a transformed organism that contains a nucleic acid encoding said peptide in an appropriate culture medium; ~~followed by extractioning~~ said peptide; and totally or partially purifyingication of the helomicine obtained said peptide.